

Figure 1

Map of Human CD20/IgE-Receptor Like cDNA (SEQ ID NO: 1) and
Amino Acid Sequence (SEQ ID NO: 2)

(Agp-96614-a1)

(CD20RP2)

5

1	TTCCAGTGCTCCAGGCAGCCTCAGCACAAGAAAAGAACATGGTCTAGACTGAAGTACCAA	60
61	CTAAATCATCTCCTTTCAAATTATCACCGACACCATCATGGATTCAAGCACCGCACACAG	120
1	M D S S T A H S	8
121	TCCGGTGTCTTCTGGTATTTCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACT	180
9	P V F L V F P P E I T A S E Y E S T E L	28
181	TTCAGCCACGACCTTTTCAACTCAAAGCCCCTTGCAAAAATTATTTGCTAGAAAAATGAA	240
29	S A T T F S T Q S P L Q K L F A R K M K	48
241	AATCTTAGGGACTATCCAGATCCTGTTTGGAATTATGACCTTTCTTTTGAGTTATCTT	300
49	I L G T I Q I L F G I M T F S F G V I F	68
301	CCTTTTCACTTTGTAAACCATATCCAAGGTTTCCCTTTATATTTCTTTTCAGGATATCC	360
69	L F T L L K P Y P R F P F I F L S G Y P	88
361	ATTCTGGGGCTCTGTTTTGTTCATTAATTCTGGAGCCTTCCTAATTGCAGTGAAAAGAAA	420
89	F W G S V L F I N S G A F L I A V K R K	108
421	AACCACAGAACTCTGATAATATTGAGCCGAATAATGAATTTTCTTAGTGCCCTGGGAGC	480
109	T T E T L I I L S R I M N F L S A L G A	128
481	AATAGCTGGAATCATTCTCCTCACATTTGGTTTCATCCTAGATCAAACTACATTTGTGG	540
129	I A G I I L L T F G F I L D Q N Y I C G	148
541	TTATTCTCACCAAAATAGTCAGTGTAAGGCTGTTACTGTCCTGTTCTTGGAATTTTGAT	600
149	Y S H Q N S Q C K A V T V L F L G I L I	168
601	TACATTGATGACTTTTCAGCATTATTGAATTATTCAATTCTCTGCCTTTCTCAATTTGGG	660
169	T L M T F S I I E L F I S L P F S I L G	188
661	GTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGACTAGCACTGTGAGAATAAAG	720
189	C H S E D C D C E Q C C *	201
721	ATGTGTTAAATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	760

Figure 2

Map of Human CD20/IgE-receptor Like cDNA (SEQ ID NO: 3) and
Amino Acid Sequence (SEQ ID NO: 4)

(Agp-69406-a1)
(CD20RP1)

1	GGCAGGAACAGCCAGTGGGAGGTTCCAGCTGAGCGCTCCCCAGAGGTGAGCTGATCCCCA	60
61	GCCACAGCACACAGGACCAGGCTGCGAGAACAGCATCATCAGCATCATGCTATTACAATC	120
1		M L L Q S 5
121	CCAAACCATGGGGGTTTCTCACAGCTTTACACCAAAGGGCATCACTATCCCTCAAAGAGA	180
6	Q T M G V S H S F T P K G I T I P Q R E	25
181	GAAACCTGGACACATGTACCAAAACGAAGATTACCTGCAGAACGGGCTGCCAACAGAAAC	240
26	K P G H M Y Q N E D Y L Q N G L P T E T	45
241	CACCGTTCTTGGGACTGTCCAGATCCTGTGTGCTGTTGATTTCAGTCTGGGGGCCAT	300
46	T V L G T V Q I L C C L L I S S L G A I	65
301	CTTGGTTTTTGTCTCCCTACCCCTCCCACTTCAATCCAGCAATTCCACCACTTTGATGTC	360
66	L V F A P Y P S H F N P A I S T T L M S	85
361	TGGGTACCCATTTTATAGGAGCTCTGTGTTTTGGCATTACTGGATCCCTCTCAATTATCTC	420
86	G Y P F L G A L C F G I T G S L S I I S	105
421	TGGAAAACAATCAACTAAGCCCTTTGACCTGAGCAGCTTGACCTCAAATGCAGTGAGTTC	480
106	G K Q S T K P F D L S S L T S N A V S S	125
481	TGTTACTGCAGGAGCAGGCCTCTTCCTCCTTGCTGACAGCATGGTAGCCCTGAGGACTGC	540
126	V T A G A G L F L L A D S M V A L R T A	145
541	CTCTCAACATTGTGGCTCAGAAATGGATTATCTATCCTCATTGCCTTATTCGGAGTACTA	600
146	S Q H C G S E M D Y L S S L P Y S E Y Y	165
601	TTATCCAATATATGAAATCAAAGATTGTCTCCTGACCAGTGTCAGTTTAACAGGTGTCCT	660
166	Y P I Y E I K D C L L T S V S L T G V L	185
661	AGTGGTGATGCTCATCTTCACTGTGCTGGAGCTCTTATTAGCTGCATACAGTTCTGTCTT	720
186	V V M L I F T V L E L L L A A Y S S V F	205
721	TTGGTGAAAACAGCTCTACTCCAACAACCCTGGGAGTTCATTTTCCTCGACCCAGTCACA	780
206	W W K Q L Y S N N P G S S F S S T Q S Q	225
781	AGATCATATCCAACAGGTCAAAAAGAGTTCTTCACGGTCTTGGATATAAGTAACTCTTGG	840
226	D H I Q Q V K K S S S R S W I *	241
841	CCTCAGAGGAAGGAAAAGCAACTCAACACTCATGGTCAAGTGTGATTAGACTTTCCTGAA	900
901	ATCTCTGCCATTTTATAGATACTGTGAAACAACTAAAAAAAAAAGCTTTTGTGTTTGTATTT	960
961	GAAAAAAAAAAAAAAAAAAAAA	982



HTM	M---ASH-E	VON---ABL-G	SASA---	HGTGSET-G	EEL-NIT---S	32
HTM	MGEFB	MHGVSRHCR	PEE---SIT-S	QAPGAPG-G	POLGMM---A	44
HURP4	M---TSQPH	PRE---TII-V	-----	WNI NF SOABK	PE-----P	29
69406	M---LLQSG	TIG---VPS	FTP-----	KG TI PORBK	PG-----H	29
1 qERbat o	M---TESNR	RAN---LAL-P	QEPSSVAF-	EVLEI SQEVS	SSGRLL---K	40
96614	M---DSTA	HSP---VFL-F	FPF-----	-EI TASEYIS	TEL-SA-T--	31
HTPEF86	MHSVSAVVP	ANSVL VAPH	NGV PV TPGI M	SNVPL VYMSQ	POV HVL RGNP	34
hCD20	MTFRHSV--	-----N	GTF PAEP- MK	GPI ANSGSK	P---LF R RM	50
HTM5F5	MDTGQA--	-----	ROVGL	-----	-----	12
HTAL6	MDVQGA--	-----	ROI GR	-----	-----	12
Conz enz w	M-----	-----	-----	-----	-----	50
HTM	VYHPI---NES	QD-YOKALKQ	VLGA-Q LNA	AM LALGIML	QV WPHFQ	79
HTM	VI HSHWKL	GVTI WGSUM	VLGVV Q LTA	UMLSMG TM	MOH-SIN YG	93
HURP4	THQOZ--DSL	KOL-HLRBK	VIGTI Q LOG	MYLSLG TM	ASAS SRIFT	76
69406	MI QIE--DYL	VLN QL PTET	VLGTV Q LCC	LII SSLGAL	VFAVPP SHFN	76
1 qERbat o	SASSPLHWT	LT-VL KKDE	FLGVT Q LTA	M OLOFQWV	OSVLD SHI E	77
96614	PT STQ--SPL	QK LF ARMK	ILGTI Q LFG	IMTFSFGIT	LFTL-LHPYP	88
HTPEF86	PSLVSNHGO	POKALKBKQ	TILGAI Q IIG	LHM GLGSH	ATVL-VGEVL	98
hCD20	SSLVG--PTQ	TF--FMRSEK	TILGAI Q MNG	LH ALGGLL	LAH ALGGL	76
HTM5F5	-SLIT--	-----L-	QVCI VANA	LLVFNK--	-TSW TM-N	41
HTAL6	-SLVG--	-----	ALLCI VANA	LLVFNK--	-TKY-ASE-N	41
Conz enz w	-----	-----E-	-LG-I Q U-	L-----G-	-----	100
HTM	KNHFFITFYT	GVI WGVAF	CSGGT LSNVA	G KP-----	-----T-	116
HTM	SH--PI SYVI	GVTI WGSUM	II SGLS LA	G RT-----	-----T-	124
HURP4	QV-TSTLINS	APFI GFIFT	II SGLS AT	DKSL	-----T-	110
69406	PA-I STILMS	GVPFL GALCF	II SGLS I S	KOS	-----T-	110
1 qERbat o	GD-I FSSFA	GVPFGAIFT	II SGLS I S	EPKRN	-----A-	123
96614	RO-FFPI FLS	GVPFVGEVL	INSGBALI AV	IRRN	-----T-	110
HTPEF86	SI SYVGF--	PF-V GGLV	II SGLS VAA	ENK	-----VS-	123
hCD20	PI OYTWV--	PL-V GGLV	II SGLS LA	ENK	-----P-	109
HTM5F5	HL SLOWHVL	GF-V GGLV	LOP G AWNA	QKQDCSAGC	QGN-----RC	85
HTAL6	HL SVFVWFS	GF-V GGLV	LLRFV ITI Q	EQDCD--GQ	QSHENGKRC	88
Conz enz w	-----	GY-----G--F	I SGL LS	-----	-----	150
HTM	-----	-----FW	I QHST GNTA	SATI ALVSTA	FLSLN AVN	147
HTM	-----	-----KEL	IVSLG GNTT	AVSAGSIL	I NTFSL AF-Y	158
HURP4	-----	-----ML	VHSL VOSI L	SALSALVGI	ILSVKQALN	143
69406	-----	-----KPF	DLSS TSNAV	SVYTAGGLF	LLADSHALR	143
1 qERbat o	-----	-----TYL	VHSL GNTA	SSI AGGIFT	ILI I NLKSL	143
96614	-----	-----ETL	II SRIPI ML	SALGAI AGI	LLTF I L DQ	143
HTPEF86	-----	-----VCL	LSGLS QLV V	SSI CSAGVH	LFI TOL-----S	161
hCD20	-----	-----KOL	VHSLVHSL	PLFAM SGN	LSI NOI LNI K	142
HTM5F5	-----	-----PMLRSWF SSA	GVILGN YCL	SVSGAGRLN	SROU GWF	130
HTAL6	-----	-----AMLSSV LAL	I G AGSSVY	I VAAK LAEG	FLODLSGVA	134
Conz enz w	-----	-----L	-----SLG N-	S-----A--G-	-----	200
HTM	QSLRSHSSS	E-----SPILC	NVMSG-----I	SN-----	-GMSL-LI	179
HTM	-SFH-H--	-P-YC	MYGN-----S	NNHGTHTIL	ML DGM-L LL	190
HURP4	PASLOQ LDK	D-N N PTRASV	SVY VHDS VT	TDOT AKAS	AGI LSL M LI	191
69406	TASOHGSEM	H-V LSSL PYS	EYVYP-V IEI	KOLL TSV SL	GLV LHM LI	190
1 qERbat o	AWI H--	-----I HSDV	KFF-----E	TKOPHAF S	TEI VHM LI	191
96614	NI W--	-----O	GVSH-----N	SOQRA	VTVLFLG LI	167
HTPEF86	I SHF--	PI-----AP	-----	-----P--Y	AGVNGP M L	183
hCD20	I SHFLAKSL	HFI RAH PVI	NI YNDPAP	SEKNSFST	QYSI QSLV LT	192
HTM5F5	TAG--	WILLNRI LND	RCE-----	AP-----P	PRV PVM V	157
HTAL6	TEG--	QYLLDS VNS	ECT-----	-----E-P-	KH VEVN VS	161
Conz enz w	-----	-----	-----Y-----	-----	-----L	250
HTM	LTLLECVTI	STI AM-----	-----WDM	-----ANON-S	-----	203
HTM	LSVLEFCI AV	SLSAF-----	-----GOK-	-----VL OCT-P	GGV LLI LP SH	224
HURP4	OTLLEFCI AV	LTWL-----	-----PMK-	-----GVSDP	GV LFL RST	224
69406	FTVLELL LAA	TSVW-----	-----GAG-	-----EE LKSN	GSSFSTSSZ	224
1 qERbat o	LTIL VL GSH	SLTI O-----	-----GAG-	-----EE LKSN	VPRVYEL	224
96614	ITLMTSII E	LFI SL-----	-----PF S-	-----I L GSH	-----	190
HTPEF86	I SGHVLVFL	LEFG-----	-----ACAS	SHF GGLV CC	-----QSNV	217
hCD20	ILSVLMI FAF	FOELV LA V	ENK WKRCSS	PKSH VLL SA	EKKKRTI EI	242
HTM5F5	LT SLLVAGC	VEI LAG V	-----C-	G GLV--	-----NAT	192
HTAL6	LF SI LLAAGG	IEFII-----	-----C-	-----LI QV--	-----NSVL	186
Conz enz w	... L L	-----	-----C-	-----	-----	300
HTM	-----	-----	-----	-----	-----	214
HTM	-----	-----	-----	-----	-----	239
HURP4	-----	-----	-----	-----	-----	248
69406	-----	-----	-----	-----	-----	240
1 qERbat o	-----	-----	-----	-----	-----	244
96614	-----	-----	-----	-----	-----	200
HTPEF86	-----	-----	-----	-----	-----	245
hCD20	-----	-----	-----	-----	-----	292
HTM5F5	-----	-----	-----	-----	-----	193
HTAL6	-----	-----	-----	-----	-----	197
Conz enz w	-----	-----	-----	-----	-----	350
HTM	-----	-----	-----	-----	-----	214
HTM	-----	-----	-----	-----	-----	239
HURP4	-----	-----	-----	-----	-----	248
69406	-----	-----	-----	-----	-----	240
1 qERbat o	-----	-----	-----	-----	-----	244
96614	-----	-----	-----	-----	-----	200
HTPEF86	-----	-----	-----	-----	-----	245
hCD20	-----	-----	-----	-----	-----	292
HTM5F5	-----	-----	-----	-----	-----	193
HTAL6	-----	-----	-----	-----	-----	197
Conz enz w	-----	-----	-----	-----	-----	350
HTM	-----	-----	-----	-----	-----	214
HTM	-----	-----	-----	-----	-----	239
HURP4	-----	-----	-----	-----	-----	248
69406	-----	-----	-----	-----	-----	240
1 qERbat o	-----	-----	-----	-----	-----	244
96614	-----	-----	-----	-----	-----	200
HTPEF86	-----	-----	-----	-----	-----	245
hCD20	-----	-----	-----	-----	-----	292
HTM5F5	-----	-----	-----	-----	-----	193
HTAL6	-----	-----	-----	-----	-----	197
Conz enz w	-----	-----	-----	-----	-----	350